

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/756,551DATE: 03/13/2001
TIME: 23:08:43

INPUT SET: S36499.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANTS: C. Morrow et al.
6
7 (ii) TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT VIRAL
8 NUCLEIC ACID AND METHODS OF MAKING AND
9 USING SAME
10
11 (iii) NUMBER OF SEQUENCES: 23
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: LAHIVE & COCKFIELD
15 (B) STREET: 28 STATE STREET
16 (C) CITY: BOSTON
17 (D) STATE: MASSACHUSETTS
18 (E) COUNTRY: USA
19 (F) ZIP: 02109
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: ASCII
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: 09/756,551
29 (B) FILING DATE:
30 (C) CLASSIFICATION:
31
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: 08/987,867
34 (B) FILING DATE:
35
36 (vii) PRIOR APPLICATION DATA:
37 (A) APPLICATION NUMBER: US 08/087,009
38 (B) FILING DATE: 01-JUL-1993
39
40 (viii) ATTORNEY/AGENT INFORMATION:
41 (A) NAME: Myers, Louis
42 (B) REGISTRATION NUMBER: 35,965
43 (C) REFERENCE/DOCKET NUMBER: UAP-004CPDV
44
45 (ix) TELECOMMUNICATION INFORMATION:
46 (A) TELEPHONE: (617) 227-7400

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47 (B) TELEFAX: (617) 742-4214
48
49
50 (2) INFORMATION FOR SEQ ID NO:1:
51
52 (i) SEQUENCE CHARACTERISTICS:
53 (A) LENGTH: 14 base pairs
54 (B) TYPE: nucleic acid
55 (C) STRANDEDNESS: single
56 (D) TOPOLOGY: linear
57
58 (ii) MOLECULE TYPE: cDNA
59
60
61
62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
63
64 TATTAGTAGA TCTG
65
66 (2) INFORMATION FOR SEQ ID NO:2:
67
68 (i) SEQUENCE CHARACTERISTICS:
69 (A) LENGTH: 14 base pairs
70 (B) TYPE: nucleic acid
71 (C) STRANDEDNESS: single
72 (D) TOPOLOGY: linear
73
74 (ii) MOLECULE TYPE: cDNA
75
76
77
78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
79
80 TACAGATGTA CTAA
81
82 (2) INFORMATION FOR SEQ ID NO:3:
83
84 (i) SEQUENCE CHARACTERISTICS:
85 (A) LENGTH: 845 base pairs
86 (B) TYPE: nucleic acid
87 (C) STRANDEDNESS: single
88 (D) TOPOLOGY: linear
89
90 (ii) MOLECULE TYPE: cDNA
91
92
93 (ix) FEATURE:
94 (A) NAME/KEY: CDS
95 (B) LOCATION: 20..845
96
97
98 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
99

14

14

RAW SEQUENCE LISTING PATENT APPLICATION US/09/756,551

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| | | |
|-----|--|-----|
| 100 | ACACAGCAAT CAGGTCAGC CAA AAT TAC CCT ATA GTG CAG AAC ATC CAG GGG | 52 |
| 101 | Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly | |
| 102 | 1 5 10 | |
| 103 | | |
| 104 | CAA ATG GTA CAT CAG GCC ATA TCA CCT AGA ACT TTA AAT GCA TGG GTA | 100 |
| 105 | Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val | |
| 106 | 15 20 25 | |
| 107 | | |
| 108 | AAA GTA GTA GAA GAG AAG GCT TTC AGC CCA GAA GTG ATA CCC ATG TTT | 148 |
| 109 | Lys Val Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe | |
| 110 | 30 35 40 | |
| 111 | | |
| 112 | TCA GCA TTA TCA GAA GGA GCC ACC CCA CAA GAT TTA AAC ACC ATG CTA | 196 |
| 113 | Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu | |
| 114 | 45 50 55 | |
| 115 | | |
| 116 | AAC ACA GTG GGG GGA CAT CAA GCA GCC ATG CAA ATG TTA AAA GAG ACC | 244 |
| 117 | Asn Thr Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr | |
| 118 | 60 65 70 75 | |
| 119 | | |
| 120 | ATC AAT GAG GAA GCT GCA GAA TGG GAT AGA GTG CAT CCA GTG CAT GCA | 292 |
| 121 | Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala | |
| 122 | 80 85 90 | |
| 123 | | |
| 124 | GGG CCT ATT GCA CCA GGC CAG ATG AGA GAA CCA AGG GGA AGT GAC ATA | 340 |
| 125 | Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile | |
| 126 | 95 100 105 | |
| 127 | | |
| 128 | GCA GGA ACT ACT AGT ACC CTT CAG GAA CAA ATA GGA TGG ATG ACA AAT | 388 |
| 129 | Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn | |
| 130 | 110 115 120 | |
| 131 | | |
| 132 | AAT CCA CCT ATC CCA GTA GGA GAA ATT TAT AAA AGA TGG ATA ATC CTG | 436 |
| 133 | Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu | |
| 134 | 125 130 135 | |
| 135 | | |
| 136 | GGA TTA AAT AAA ATA GTA AGA ATG TAT AGC CCT ACC AGC ATT CTG GAC | 484 |
| 137 | Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp | |
| 138 | 140 145 150 155 | |
| 139 | | |
| 140 | ATA AGA CAA GGA CCA AAG GAA CCC TTT AGA GAC TAT GTA GAC CGG TTC | 532 |
| 141 | Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe | |
| 142 | 160 165 170 | |
| 143 | | |
| 144 | TAT AAA ACT CTA AGA GCC GAG CAA GCT TCA CAG GAG GTA AAA AAT TGG | 580 |
| 145 | Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp | |
| 146 | 175 180 185 | |
| 147 | | |
| 148 | ATG ACA GAA ACC TTG TTG GTC CAA AAT GCG AAC CCA GAT TGT AAG ACT | 628 |
| 149 | Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr | |
| 150 | 190 195 200 | |
| 151 | | |
| 152 | ATT TTA AAA GCA TTG GGA CCA GCG GCT ACA CTA GAA GAA ATG ATG ACA | 676 |

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153 Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr
154      205                      210                      215
155
156 GCA TGT CAG GGA GTA GGA GGA CCC GGC CAT AAG GCA AGA GTT TTG GCT      724
157 Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala
158 220                      225                      230                      235
159
160 GAA GCA ATG AGC CAA GTA ACA AAT TCA GCT ACC ATA ATG ATG CAG AGA      772
161 Glu Ala Met Ser Gln Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg
162                      240                      245                      250
163
164 GGC AAT TTT AGG AAC CAA AGA AAG ATT GTT AAG TGT TTC AAT TGT GGC      820
165 Gly Asn Phe Arg Asn Gln Arg Lys Ile Val Lys Cys Phe Asn Cys Gly
166                      255                      260                      265
167
168 AAA GAA GGG CAC ACA GCC AGA AAG T      845
169 Lys Glu Gly His Thr Ala Arg Lys
170      270                      275
171
172
173 (2) INFORMATION FOR SEQ ID NO:4:
174
175 (i) SEQUENCE CHARACTERISTICS:
176 (A) LENGTH: 275 amino acids
177 (B) TYPE: amino acid
178 (D) TOPOLOGY: linear
179
180 (ii) MOLECULE TYPE: protein
181
182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
183
184 Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His Gln
185 1                      5                      10                      15
186
187 Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu
188      20                      25                      30
189
190 Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu
191      35                      40                      45
192
193 Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly
194      50                      55                      60
195
196 His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala
197      65                      70                      75                      80
198
199 Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro
200      85                      90                      95
201
202 Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser
203      100                      105                      110
204
205 Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro

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206          115          120          125
207
208 Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile
209      130          135          140
210
211 Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro
212 145          150          155          160
213
214 Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg
215          165          170          175
216
217 Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu
218          180          185          190
219
220 Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu
221      195          200          205
222
223 Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val
224      210          215          220
225
226 Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln
227 225          230          235          240
228
229 Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg Asn
230          245          250          255
231
232 Gln Arg Lys Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Thr
233      260          265          270
234
235 Ala Arg Lys
236      275
237
238 (2) INFORMATION FOR SEQ ID NO:5:
239
240 (i) SEQUENCE CHARACTERISTICS:
241 (A) LENGTH: 948 base pairs
242 (B) TYPE: nucleic acid
243 (C) STRANDEDNESS: single
244 (D) TOPOLOGY: linear
245
246 (ii) MOLECULE TYPE: cDNA
247
248
249 (ix) FEATURE:
250 (A) NAME/KEY: CDS
251 (B) LOCATION: 4..946
252
253
254 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
255
256 AAC CAA TGG CCA TTG ACA GAA GAA AAA ATA AAA GCA TTA GTA GAA ATT
257 Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile
258      1          5          10          15

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PAGE: 1

SEQUENCE VERIFICATION REPORT
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| Line | Error | Original Text |
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